



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 160722

TO: Mark Shibuya
Location: REM-2A10&2C18
Art Unit: 1639
Monday, August 01, 2005

Case Serial Number: 09/667237

From: Edward Hart
Location: Biotech-Chem Library
REM-1A55
Phone: 571-272-2512

edward.hart@uspto.gov

Search Notes

Examiner Shibuya,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart



This Page Blank (uspto)

160722

From: Shibuya, Mark
Sent: Wednesday, July 27, 2005 2:30 PM
To: STIC-Biotech/ChemLib
Subject: Search req. for SEQ NO:12 of 09/667,237.

Please search SEQ NO:12 of 09/667,237.

This case is before the first action on the merits.

Mark Shibuya
Art Unit 1639, Remsen 2a10, ext: 2-0806

CRP

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: 7/29/05
Date Completed: 8/1/05
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA#: 1 AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: 21
WWW/Internet: _____
Other(Specify): _____

This Page Blank (uspto)



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact*:

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library, Remsen Bldg.



This Page Blank (uspto)

RESULT 6	BX470087/c	218404 bp	DNA	linear	VRT 26-FEB-2004	
LOCUS	Zebrafish DNA sequence from clone CH211-202A10 in linkage group 3, complete sequence.					
DEFINITION	BX470087					
ACCESSION	BX470087.8 GI:43823873					
VERSION	HTG.					
KEYWORDS	Danio rerio (zebrafish)					
SOURCE	Danio rerio					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.					
REFERENCE	1 (bases 1 to 218404)					
AUTHORS	Pelán,S.					
TITLE	Direct Submission					
JOURNAL	Submitted (26-FEB-2004) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk					
COMMENT	On Feb 26, 2004 this sequence version replaced gi:42820884. ----- Genome Center Center: Wellcome Trust Sanger Institute Center code: SC Web site: http://www.sanger.ac.uk Contact: zfish-help@sanger.ac.uk ----- During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems; such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep Clone-derived Zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be submitted. Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'dr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see http://www.sanger.ac.uk/Projects/D_rerio/fishmask.shtml CH211-202A10 is from a CHORI-211 BAC library VECTOR: pTARBAC2.1.					
FEATURES	Location/Qualifiers 1. .218404 /organism="Danio rerio" /mol_type="genomic DNA" /db_xref="taxon:7955" /clone="CH211-202A10" /clone_lib="CHORI-211"					
ORIGIN						
Query Match	79.5%	Score 31;	DB 5;	Length 218404;		
Best Local Similarity	87.2%	Pred. No. 2;				
Matches	34;	Conservative	0;	Mismatches	5;	
			Indels	0;	Gaps	0;
QY	1 ACTACTGCTACTGGTCTAGTACTACTGCTGGTGGTCTAGT 39 					
Db	28923 ACTACTACTACTGCTACTACTACTACTGCTGCTGCTACT 28885 					

AUTHORS Rat Genome Sequencing Consortium.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On May 13, 2003 this sequence version replaced gi:23268918. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: <http://www.hgsc.bcm.tmc.edu/>
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GIWC
Center clone name: CH230-69L10
----- Summary Statistics
Assembly program: Atlas 3.0;
Consensus quality: 213355 bases at least Q40
Consensus quality: 219597 bases at least Q30
Consensus quality: 223913 bases at least Q20
Estimated insert size: 225595; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
* 1 239825: contig of 239825 bp in length
* 239826 239925: gap of unknown length
* 239926 241173: contig of 1248 bp in length.
FEATURES
source Location/Qualifiers
1. .241173
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-69L10"
misc_feature 1. .1631
/note="wgs contig"
misc_feature 31777. .32772
/note="wgs contig"
misc_feature 101829. .103618
/note="wgs contig"
misc_feature 193630. .194760
/note="wgs contig"
misc_feature 226377. .227570
/note="wgs_contig"
ORIGIN
Query Match 79.5%; Score 31; DB 2; Length 241173;
Best Local Similarity 87.2%; Pred. No. 1.9;
Matches 34; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 39
|||||
Db 21848 ACTACTGCTACTGCTACTGCTACTGCTACTGCTGCTACT 21810
|||||

RESULT 8
BV090840
LOCUS 402 bp DNA linear STS 15-OCT-2003
DEFINITION RPAMMSEQ0002739 Roche Palo Alto Mus musculus STS genomic, sequence tagged site.
ACCESSION BV090840
VERSION BV090840.1 GI:37668319
KEYWORDS STS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 402)
USUKA,J., Liao,G., Cheng,J., Nguyen,A., Bach,C., Puech,A., McPherson,J.D., Foernzler,D. and Peltz,G.
Mus musculus SNPs
Unpublished (2003)
COMMENT Contact: Jonathan Usuka
Roche Palo Alto Genetics and Genomics Department
Roche Palo Alto
3431 Hillview Ave, Mailstop S3-1, Palo Alto, CA 94024, USA
Tel: 6508555807
Email: Jonathan.Usuka@roche.com
Primer A: No primer submitted
Primer B: No primer submitted.
Location/Qualifiers
1. .402
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/map="7-144325-144544-AC087063.20.1.241381"
/clone_lib="Roche Palo Alto"
/note="SNPs developed from assay sequences derived from 15 different strains-of mice (as of October 1, 2003). Those strains include A/J, A/HeJ, -129/Sv, AKR/J, B10.D2-H2/OSnJ, BALB/cByJ, BALB/cJ, C3H/HeJ, C57BL/6J, -CAST/Ei, DBA/2J, MRL/MpJ, NZB/BinJ, NZW/LaC, SPRET/Ei.-"
<1. .>402
STS
ORIGIN
Query Match 76.9%; Score 30; DB 11; Length 402;
Best Local Similarity 86.8%; Pred. No. 6.6;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 CTACTGCTACTGGTCTAGTACTACTGCTGCTGCTAGT 39
|||||
Db 169 CTGCTGCTGCTGGTGGTAGTATTCTGCTGCTGCTAGT 206
|||||
RESULT 9
AF329581
LOCUS 410 bp DNA linear INV 15-MAR-2001
DEFINITION Plasmodium falciparum genotype 3 from Solomon Islands merozoite surface protein 2 gene, partial cds.
ACCESSION AF329581
VERSION AF329581.1 GI:13345560
KEYWORDS
SOURCE Plasmodium falciparum (malaria parasite P. falciparum)
ORGANISM Plasmodium falciparum
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 410)
EISEN,D.P., Cloonan,N., Baddeley,A., Eri,R. and Saul,A.
Antigenic drift and immune selection acting on merozoite surface protein 1-19 and merozoite surface protein 2 in independent field isolates of Plasmodium falciparum
Unpublished
2 (bases 1 to 410)
EISEN,D.P., Cloonan,N., Baddeley,A., Eri,R. and Saul,A.
Direct Submission
Submitted (19-DEC-2000) Infectious Diseases, Royal Brisbane Hospital, Herston Rd., Herston, QLD 4029, Australia

FEATURES	source	Location/Qualifiers										
		1. .410										
		/organism="Plasmodium falciparum"										
		/mol_type="genomic DNA"										
		/db_xref="taxon:5833"										
		/chromosome="2"										
		/country="Solomon Islands"										
		/note="genotype: 3"										
		<1. .>410										
		/product="merozoite surface protein 2"										
mRNA	CDS	<1. .>410										
		/codon_start=1										
		/product="merozoite surface protein 2"										
		/protein_id="AAK19400.1"										
		/db_xref="GI:13345561"										
		/translation="ENIKNESKYSNTFINNAYNMSIRRSMTESKTPTPTGAGAGAGAS										
		GSAGSGDASGSAGSAGSAGSAGSAGSAGSAGSAGSAGSPSTPATTTTTTTTND										
		EASTSTSSENPNHNNAKTNPKNGGVQKPNQANK"										
ORIGIN												
	Query Match 76.9%; Score 30; DB 3; Length 410;											
	Best Local Similarity 86.8%; Pred. No. 6.6;											
	Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;											
	2 CTACTGCTACTGGTGCTAGTACTACTGCTGGTGCTAGT 39											
	95 CTACTCCTACTGGTGCTGGTGCTGGTGCTGGTGCTAGT 132											
RESULT 10	AY375168	LOCUS	Plasmodium falciparum merozoite surface protein 2 (msp2) gene,									
			msp2-B allele, partial cds.									
			AY375168									
			AY375168.1 GI:34863456									
			Plasmodium falciparum (malaria parasite P. falciparum)									
			Plasmodium falciparum									
			Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.									
			1 (bases 1 to 558)									
			Felger,I., Steiger,S., Hatz,C., Smith,T. and Beck,H.-P.									
			Antigenic cross-reactivity between different alleles of the									
REFERENCE	AUTHORS	TITLE	Plasmodium falciparum merozoite surface protein 2									
			Parasite Immunol. 25 (11-12), 531-543 (2003)									
			2 (bases 1 to 558)									
			Felger,I.									
			Direct Submission									
			Submitted (28-AUG-2003) MPI, Swiss Tropical Institute, Socinstrasse									
			57, Basel CH-4002, Switzerland									
			Location/Qualifiers									
			1. .558									
			/organism="Plasmodium falciparum"									
gene	mRNA	CDS	/mol_type="genomic DNA"									
			/db_xref="taxon:5833"									
			/chromosome="2"									
			/note="field isolate"									
			<1. .>558									
			/gene="msp2"									
			/allele="B"									
			<1. .>558									
			/gene="msp2"									
			/allele="B"									
/product="merozoite surface protein 2"												
<1. .>558												
/gene="msp2"												
/allele="B"												
/codon_start=2												
/product="merozoite surface protein 2"												
/protein_id="AAQ82917.1"												
/db_xref="GI:34863457"												
/translation="SIRRSMTESKTPTPTGAGAGAGSAGSGDGASGSAGSAGSAGAS												
GSAGSGSAGSAGSAGSAGSPSTPATTTTTTTTNDAAESTSTSSENPNHNNAKTNP												

Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A., Mangun,B., Mapua,P., Martin,K., Martin,R., Martinec,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.

Direct Submission
 Unpublished
 2 (bases 1 to 255613)
 Worley,K.C.
 Direct Submission
 Submitted (06-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 255613)
 Rat Genome Sequencing Consortium.
 Direct Submission
 Submitted (15-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Nov 15, 2002 this sequence version replaced gi:23267317.
 The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: <http://www.hgsc.bcm.tmc.edu/>
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GTLL
 Center clone name: CH230-123D20
 ----- Summary Statistics
 Assembly program: Phrap; version 0.990329
 Consensus quality: 214418 bases at least Q40
 Consensus quality: 218498 bases at least Q30
 Consensus quality: 221512 bases at least Q20
 Estimated insert size: 220593; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 7122: contig of 7122 bp in length
 * 7123 7222: gap of unknown length
 * 7223 236393: contig of 229171 bp in length
 * 236394 236493: gap of unknown length
 * 236494 239610: contig of 3117 bp in length
 * 239611 239710: gap of unknown length
 * 239711 254301: contig of 14591 bp in length
 * 254302 254401: gap of unknown length
 * 254402 255613: contig of 1212 bp in length.
 FEATURES
 source
 1..255613
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-123D20"
 1..1707
 /note="wgs_end_extension
 clone_end:T7"
 5513..6417
 /note="clone_boundary
 clone_end:T7
 site:
 end_sequence:BH295470"
 34541..35596
 /note="wgs_contig"
 226717..227629
 /note="clone_boundary
 clone_end:Sp6
 site:
 end_sequence:BH295472"
 229888..232421
 /note="wgs_end_extension
 clone_end:Sp6"
 239711..242291
 /note="wgs_end_extension
 clone_end:Sp6"
 242342..243499
 /note="wgs_end_extension
 clone_end:Sp6"
 ORIGIN
 Query Match 76.9%; Score 30; DB 2; Length 255613;
 Best Local Similarity 86.8%; Pred.No. 4.2;
 Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 2 CTACTGCTACTGGTGTAGTAGTACTACTGCTGGTGTAGT 39
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 62002 CTACTACTACTGCTGTACTACTACTACTGCTGTACT 62039

Search completed: July 30, 2005, 07:40:53
 Job time : 1564 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 05:48:49 ; Search time 270 Seconds
(without alignments)
855.074 Million cell updates/sec

Title: US-09-667-237B-12
Perfect score: 39
Sequence: 1 actactgctactggtgtagtactactgctggtgtagt 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4390206 seqs, 2959870667 residues
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	39	100.0	39	4	AAH20260	Aah20260 CJ linker
2	39	100.0	39	4	AAS45570	Aas45570 B cell ly
3	39	100.0	39	8	ACD40364	Acd40364 DNA encod
4	39	100.0	39	9	ACD06879	Acd06879 Immunogen
5	39	100.0	39	9	ACD06137	Acd06137 Immunogen
6	39	100.0	39	9	ACD45089	Acd45089 DNA encod
7	30	76.9	109453	13	ABD32728	Abd32728 Mouse can
8	29	74.4	2059	12	ADG73739	Adg73739 Aspergill
9	29	74.4	3438	4	AAH62788	Aah62788 Shrimp wh
10	29	74.4	305107	4	AAH62689	Aah62689 Shrimp wh
11	28.6	73.3	204803	12	ADQ97348	Adq97348 Mouse can
12	28.4	72.8	39	4	AAH20262	Aah20262 CJ linker
13	28.4	72.8	39	4	AAS45572	Aas45572 B cell ly
14	28.4	72.8	39	8	ACD40366	Acd40366 DNA encod
15	28.4	72.8	39	9	ACD06881	Acd06881 Immunogen
16	28.4	72.8	39	9	ACD06139	Acd06139 Immunogen
17	28.4	72.8	39	9	ACD45091	Acd45091 DNA encod
18	27.8	71.3	488	9	ACH32706	Ach32706 Human end
19	27.8	71.3	495	10	ADF85490	Adf85490 Human ade
20	27.8	71.3	544	12	ACH89611	Ach89611 Human gen

C	21	27.8	71.3	553	6	ABK45910	Abk45910 CDNA enco
	22	27.8	71.3	586	12	ACH75899	Ach75899 Human gen
	23	27.8	71.3	864	2	AAQ03877	Aaq03877 Merozoite
C	24	27.8	71.3	1326	5	AAS83104	Aas83104 DNA encod
C	25	27.8	71.3	3376	2	AAQ75166	Aaq75166 AF-9 CDNA
C	26	27.8	71.3	3376	10	ADK67000	Adk67000 Gene #90
	27	27.8	71.3	45764	12	ADQ97275	Adq97275 Mouse can
C	28	27.4	70.3	789	3	AAC51118	Aac51118 Arabidops
C	29	27.4	70.3	1053	3	AAC34958	Aac34958 Arabidops
C	30	27.4	70.3	1054	3	AAC51122	Aac51122 Arabidops
C	31	27.4	70.3	1092	3	AAC41597	Aac41597 Arabidops
C	32	27.4	70.3	1095	3	AAC33089	Aac33089 Arabidops
C	33	27.4	70.3	1095	3	AAC51124	Aac51124 Arabidops
C	34	27.4	70.3	1452	3	AAC36250	Aac36250 Arabidops
C	35	27.4	70.3	1453	3	AAC51120	Aac51120 Arabidops
	36	27	69.2	45	10	ADE78398	Ade78398 DNA encod
	37	27	69.2	819	2	AAQ03876	Aaq03876 Merozoite
C	38	27	69.2	2510	13	ADR25170	Adr25170 Breast ca
C	39	27	69.2	3277	12	ADQ17646	Adq17646 Human sof
C	40	27	69.2	3341	10	ADF81653	Adf81653 Leukaemia
	41	26.8	68.7	60	4	AAH20265	Aah20265 CJ linker
	42	26.8	68.7	60	4	AAS45575	Aas45575 B cell ly
	43	26.8	68.7	60	8	ACD40369	Acd40369 DNA encod
	44	26.8	68.7	60	9	ACD06884	Acd06884 Immunogen
	45	26.8	68.7	60	9	ACD06142	Acd06142 Immunogen

ALIGNMENTS

RESULT 1
AAH20260
ID AAH20260 standard; DNA; 39 BP.
XX
AC AAH20260;
XX
DT 27-JUL-2001 (first entry)
XX
DE CJ linker library oligonucleotide sequence SEQ ID 12.
XX
KW Polynucleotide library; dual-domain; linker; vaccine; B-cell lymphoma;
KW ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..39
FT /*tag= a
FT /partial
FT /product= "Linker"
FT /note= "No stop or start codon given"
XX
PN WO200123543-A1.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US025965.
XX
PR 24-SEP-1999; 99US-0155978P.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX
PI Reintl SJ, Lindbo JA, Turpen T;
XX
DR WPI; 2001-316135/33.
XX
PT P-PSDB; AAB97244.
XX
PT Novel library of dual-domain nucleic acid molecules useful for producing
PT dual-domain proteins, or idiotypic scFv vaccine useful for treating B-
XX cell lymphoma.
PS Example 1; Page 34; 77pp; English.
XX

	Matches	39;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	ACTACTGCTACTGGTGTAGTAGTACTACTGCTGGTGCTAGT	39							
Db	1	ACTACTGCTACTGGTGTAGTAGTACTACTGCTGGTGCTAGT	39							

RESULT 4
ACD06879
ID ACD06879 standard; DNA; 39 BP.
XX
XX ACD06879;
XX
DT 06-AUG-2003 (first entry)
XX
DE Immunogenic single chain antibody polypeptide (scfv) linker DNA #1.
XX
KW Tumour; immunoglobulin variable region; anti-tumour; cytostatic; vaccine;
KW self-antigen; tumour-specific vaccine; B-cell lymphoma-specific vaccine;
KW B-cell lymphoma; PCR; primer; ss; single chain antibody polypeptide.
XX
OS Homo sapiens.

Novel polypeptide self-antigen useful as tumor-specific vaccine in mammals, is produced in plants and mimics one or more epitopes of antigen uniquely expressed by cells of tumor.

Example 2: Page 21: 47pp: English.

The invention describes a polypeptide self-antigen (I) useful as a tumour-specific vaccine in a subject with a tumour or at risk of developing a tumour, encoded by a nucleic acid (NA) in the cells of the tumour, including an epitope to, or overexpressed by tumour cells; produced in a cell or organism that has been transfected with NA and in a correctly folded form; and capable of inducing an immune response in a mammal. (I) is useful as a tumour-specific vaccine, especially a B-cell lymphoma-specific vaccine. A vaccine is useful for inducing a tumour-specific immune antibody response in a tumour-bearing subject, preferably human or a subject who had a tumour and was treated so that no tumour is clinically or radiographically evident, where the tumour is B-cell lymphoma. This sequence represents a primer used to isolate DNA encoding tumour associated single chain antibody polypeptides

Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;

RESULT 5
ACD06137
ID ACD06137 standard; DNA; 39 BP.
XX
XX AC ACD06137;
XX
XX DT 06-AUG-2003 (first entry)
XX
XX DE Immunogenic single chain antibody polypeptide (scfv) linker DNA #1.
XX
XX KW Tumour; immunoglobulin variable region; anti-tumour; cytostatic; vaccine;
KW inducer of immune response; self-antigen; B-cell lymphoma;
KW tumour-specific vaccine; single chain antibody polypeptide; linker; ds.
KW

Novel polypeptide self-antigen useful as tumor-specific vaccine in mammals, is produced in plants and mimics one or more epitopes of antigen uniquely expressed by cells of tumor.

Example 2: Page 23: 37pp; English.

The invention describes a polypeptide self-antigen (I) useful as a tumour-specific vaccine in a subject with a tumour or at risk of developing a tumour, encoded by a nucleic acid in the cells of the tumour, including an epitope to, or overexpressed by tumour cells; produced in a cell or organism that has been transfected with nucleic acid and in a correctly folded form; and capable of inducing an immune response in a mammal. (I) is useful as a tumour-specific vaccine, especially a B-cell lymphoma-specific vaccine. A vaccine composition is useful for inducing a tumour-specific immune antibody response in a tumour-bearing subject, preferably human or a subject who had a tumour and was treated so that no tumour is clinically or radiographically evident, where the tumour is B-cell lymphoma. This sequence encodes a linker peptide associated with single chain antibody polypeptides which function to join the variable heavy and variable light chain encoding DNA's together forming the single chain antibody

RESULT 6
ACD45089
ID ACD45089 standard; DNA; 39 BP.
XX
AC ACD45089;

XX 10-SEP-2003 (first entry)
DT DNA encoding self-antigen vaccine associated linker peptide #1.
XX
DE Self-antigen; tumour-specific vaccine; tumour; immune response;
KW anti-tumour immune response; vaccine; B-cell lymphoma;
KW transient viral expression; transgenic plant;
KW variable region gene fragment; linker; ds.
XX
OS Synthetic.
XX
PN US2003039659-A1.
XX
PD 27-FEB-2003.
XX
PF 08-FEB-2002; 2002US-00067892.
XX
PR 24-SEP-1999; 99US-0155979P.
PR 10-MAR-2000; 2000US-00522900.
XX
PA (MCCO/) MCCORMICK A A.
PA (TUSE/) TUSE D.
PA (REIN/) REINL S J.
PA (LIND/) LINDBO J A.
PA (TURP/) TURPEN T H.
XX
PI McCormick AA, Tuse D, Reinl SJ, Lindbo JA, Turpen TH;
XX
XX WPI; 2003-492153/46.
DR P-PSDB; ABO27245.
XX
PT Novel polypeptide antigen which includes epitope overexpressed by tumor
PT cells e.g. B-cell lymphoma, and is capable of inducing immune response in
PT mammal without need for adjuvant, useful as anti-tumor vaccine component.
XX
PS Example 2; Page 21; 48pp; English.
XX
CC The invention describes a polypeptide self-antigen (I) useful as tumour-
CC specific vaccine in subject with a tumour, including an epitope or
CC epitope unique to, or overexpressed by, cells of the tumour, is produced
CC in a cell or organism that has been transformed or transfected with the
CC nucleic acid derived from the tumour of subject, and is capable of
CC inducing an immune response in a mammal without a need for adjuvant or
CC other immunostimulatory materials. (I) is useful for inducing an immune
CC response, preferably a protective anti-tumour immune response in a
CC mammal, preferably human. A vaccine composition comprising (I) is useful
CC for inducing a tumour-specific immune antibody response in a tumour-
CC bearing subject (preferably human) or a subject who had a tumour and was
CC treated so that no tumour is clinically radiographically evident. The
CC vaccines are preferably useful for inducing immune antibody response
CC against B-cell lymphoma. The polypeptide is produced without the need for
CC denaturation or renaturation. (I) is rapidly produced in plants by
CC transient viral expression. Plant samples expressing the desired protein
CC can be positively identified by both enzyme linked immunosorbent assay
CC (ELISA) and Western blotting 4 weeks after molecular cloning. Thus, (I)
CC is expressed rapidly and easily in plants. This sequence encodes a self-
CC antigen associated linker peptide
XX
SQ Sequence 39 BP; 7 A; 9 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 39; DB 9; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTAGTAGTACTACTGCTGGTGTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTAGTACTACTGCTGGTGTAGT 39
|||||

RESULT 7
ABD32728
ID ABD32728 standard; DNA; 109453 BP.

XX ABD32728;
AC
XX
DT 18-NOV-2004 (first entry)
XX
DE Mouse cancer-associated genomic DNA MD15-016.
XX
KW Mouse; ds; cancer-associated protein; gene; cytostatic; cancer;
KW leukaemia; lymphoma; CAP.
XX
OS Mus musculus.
XX
PN WO2004074320-A2.
XX
PD 02-SEP-2004.
XX
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-00388838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Morris DW, Malandro MS;
XX
XX WPI; 2004-652914/63.
DR
XX
PT New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
PS disclosure; seqid 313; 310pp; English.
XX
CC The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells (comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukaemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a mouse CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 109453 BP; 29132 A; 25085 C; 24613 G; 30623 T; 0 U; 0 Other;

Query Match 76.9%; Score 30; DB 13; Length 109453;

DT 11-SEP-2001 (first entry)
XX Shrimp white spot Bacilliform virus (WSBV) genomic sequence.
DE
XX
KW Shrimp white spot Bacilliform virus; WSBV; diagnosis; viral infection;
KW antiviral agent; gene expression; antisense construct;
KW transgenic viral resistant shrimp; ds.
XX
OS Shrimp white spot syndrome virus.
XX
XX
PN WO200138351-A2.
XX
PD 31-MAY-2001.
XX
PF 08-NOV-2000; 2000WO-US028888.
XX
PR 24-NOV-1999; 99CN-00124717.
XX
PA (PENY-) PE CORP NY.
PA (THIR-) THIRD INST OCEANOGRAPHY STATE OCEANI C A.
PA (SINO-) SINOGENOMAX CO LTD.
XX
PI Xu X, Yang F, He J, Pham L, He M, Ye Y, Shen Y, Kodira C;
XX WPI; 2001-355877/37.
DR
XX Primary nucleotide sequence of the shrimp white spot Bacilliform virus
PT (WSBV), useful for producing viral polypeptides that can be used to
PT screen for agents that are useful for treating WSBV infection.
XX
PS Disclosure; Fig 2; 626pp; English.
XX
CC The invention provides the primary nucleotide sequence of the WSBV genome
CC (AAH62689), predicted transcript sequences (AAH62689-AAH62839) and
CC encoded proteins (AAG84910-AAG85051) and oligonucleotide sequences
CC (AAH62840-63160) suitable for use as primers or probes. The nucleic acid
CC molecules and proteins of the invention are useful for diagnosis and
CC monitoring viral infection, in screens for antiviral agents and for
CC monitoring viral gene expression or activity during a treatment regimen.
CC The nucleic acid molecules are also useful as antisense constructs to
CC control viral gene expression in infected cells and tissues and to create
CC transgenic viral resistant shrimp. (Updated on 06-AUG-2003 to correct OS
CC field.)
XX
SQ Sequence 305107 BP; 92042 A; 62482 C; 62635 G; 87948 T; 0 U; 0 Other;

Query Match 74.4%; Score 29; DB 4; Length 305107;
Best Local Similarity 86.5%; Pred. No. 5.5;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTA 37
Db |||||
44222 ACTGCTGCTACTGCTGCTACTACTGCTGCTGCTGCTA 44186

RESULT 11
ADQ97348/c
ID ADQ97348 standard; DNA; 204803 BP.
XX
AC ADQ97348;
XX
DT 07-OCT-2004 (first entry)
XX
DE Mouse cancer associated sequence MD08-036, SEQ ID 325.
XX
KW Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds.
XX Mus musculus.
OS
XX
PN WO2004060304-A2.
XX
PD 22-JUL-2004.
XX

PF 22-DEC-2003; 2003WO-US041389.
XX
PR 27-DEC-2002; 2002US-00330773.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX Morris DW, Malandro MS;
PI WPI; 2004-543781/52.
XX
DR
XX New isolated cancer associated nucleic acids comprising at least 10
PT contiguous nucleotides, useful for diagnosing, preventing and/or treating
PT cancers such as leukemia and lymphoma.
XX
PS Claim 1; SEQ ID NO 325; 199pp; English.
XX
CC The present invention relates to cancer associated sequences (ADQ97025-
CC ADQ98004). The sequences are useful for the diagnosis, prevention and/or
CC treatment of cancer, such as leukemia and lymphoma. Note: The sequence
CC data for this patent did not form part of the printed specification, but
CC was obtained in electronic formate directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 204803 BP; 55167 A; 44951 C; 46757 G; 55510 T; 0 U; 2418 Other;

Query Match 73.3%; Score 28.6; DB 12; Length 204803;
Best Local Similarity 88.6%; Pred. No. 7.2;
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 CTACTGCTACTGGTGTAGTACTACTGCTGGTGCT 36
Db |||||
92554 CTACTGCTACTGCTGCTACTGCTACTGCTGCTGCT 92520

RESULT 12
AAH20262
ID AAH20262 standard; DNA; 39 BP.
XX
AC AAH20262;
XX
DT 27-JUL-2001 (first entry)
XX
DE CJ linker library oligonucleotide sequence SEQ ID 16.
XX
KW Polynucleotide library; dual-domain; linker; vaccine; B-cell lymphoma;
KW ds.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT CDS 1..39
FT /*tag= a
FT /partial
FT /product= "Linker"
FT /note= "No stop or start codon given"
XX
PN WO200123543-A1.
XX
PD 05-APR-2001.
XX
PF 22-SEP-2000; 2000WO-US025965.
XX
PR 24-SEP-1999; 99US-0155978P.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
XX Reinl SJ, Lindbo JA, Turpen T;
PI WPI; 2001-316135/33.
XX P-PSDB; AAB97231.
XX
PT Novel library of dual-domain nucleic acid molecules useful for producing B-
dual-domain proteins, or idiotypic scFv vaccine useful for treating B-

PT cell lymphoma.
XX Example 1; Page 34; 77pp; English.
PS
XX This invention relates to a library of dual-domain nucleic acid
CC molecules. The two domains in the molecules are separated and linked by a
CC linker which is a member of a randomised library of linkers. The linkers
CC in the library vary in size and nucleotide sequence and consist of a
CC repeated pattern of degenerate repeated triplet nucleotides. Included in
CC the invention is a method for the production of the library. The library
CC is useful for producing dual-domain proteins of interest that have
CC therapeutic value, e.g., idiotype scFv vaccine for treating B-cell
CC lymphomas. The present sequence represents a linker oligonucleotide
CC sequence generated in an example illustrating the invention. The example
CC concerns the generation of a tumour antigen from a patient that includes
CC the idiotype of CJ B cell lymphoma
XX
SQ Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;

Query Match 72.8%; Score 28.4; DB 4; Length 39;
Best Local Similarity 84.2%; Pred. No. 4.3;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CTACTGCTACTGGTGTAGTACTACTGCTGCTGGTGTAGT 39
||||| | | | | | | | | | | | | | | | | | | | |
Db 2 CTACTGGTGCTAGTACTAGTGTACTGCTGCTGGTGTAGT 39

RESULT 13
AAS45572
ID AAS45572 standard; DNA; 39 BP.
XX
AC AAS45572;
XX
DT 18-DEC-2001 (first entry)
XX
DE B cell lymphoma CJ linker library, linker nucleotide sequence #3.
XX
KW Human; B cell lymphoma; cytostatic; immunostimulator; self-antigen;
KW tumour-specific vaccine; tumour; polyclonal immune response;
KW idiotype-specific anti-lymphoma immune response; PCR primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO200168682-A1.
XX
PD 20-SEP-2001.
XX
PF 13-OCT-2000; 2000WO-US028362.
XX
PR 10-MAR-2000; 2000US-00522900.
XX
PA (LARG-) LARGE SCALE BIOLOGY CORP.
PA (MCCO/) MCCORMICK A A.
PA (TUSE/) TUSE D.
XX
PI Reinl SJ, Turpen TH;
XX
DR WPI; 2001-596903/67.
DR P-PSDB; AAU29014.
XX
PT Novel polypeptide vaccine produced in plants, useful for inducing an
PT immune response to a self-antigen on the surface of certain tumor cells.
XX
PS Example 2; Page 59; 89pp; English.
XX
CC The invention relates to a novel polypeptide self-antigen (I) useful as a
CC tumour-specific vaccine in a subject with a tumour or at risk of
CC developing a tumour. (I) includes an epitope or epitopes unique to, or
CC over expressed by, cells of the tumour, thereby distinguishing the tumour
CC from all other tumours of the same or different histological type, or in
CC the subject or in another member of the subject's species. (I) is

CC epitopes in their native form. (I) is capable of inducing an immune
CC response in a mammal, when used as an individual-specific immunogenic
CC product comprising (I); and as a vaccine composition useful for inducing
CC a tumour-specific immune response, idiotype-specific anti-lymphoma immune
CC response, a polyclonal immune response to at least one idiotype of a
CC surface immunoglobulin or a polyclonal immune response to an idiotype.
CC The vaccine composition is useful for inducing a tumour-specific immune
CC antibody response in a tumour-bearing subject or a subject who had a
CC tumour e.g. B-cell lymphoma, and was treated so that no tumour is
CC clinically or radiographically evident. (I) is useful for inducing a
CC protective antitumour immune response. (I) can be produced at high
CC levels, is easy to purify and can be appropriately folded to mimic the
CC conformation of the native epitopes displayed at the tumour cell surface.
CC AAS45529-AAS45579 represent B cell lymphoma self antigen vaccine linker
CC sequences and PCR primers of the invention
XX
SQ Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;

Query Match 72.8%; Score 28.4; DB 4; Length 39;
Best Local Similarity 84.2%; Pred. No. 4.3;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 CTACTGCTACTGGTGTAGTACTACTGCTGCTGGTGTAGT 39
||||| | | | | | | | | | | | | | | | | | | | |
Db 2 CTACTGGTGCTAGTACTAGTGTACTGCTACTGCTGGTGTAGT 39

RESULT 14
ACD40366
ID ACD40366 standard; DNA; 39 BP.
XX
AC ACD40366;
XX
DT 03-SEP-2003 (first entry)
XX
DE DNA encoding CJ heavy chain variable region linker #3.
XX
KW Gene; ds; gene therapy; vaccine; tumour; immunoglobulin V; IgV;
KW CJ heavy chain; variable region; linker.
XX
OS Synthetic.
XX
PN US2003035807-A1.
XX
PD 20-FEB-2003.
XX
PF 08-FEB-2002; 2002US-00067790.
XX
PR 24-SEP-1999; 99US-0155979P.
PR 10-MAR-2000; 2000US-00522900.
XX
PA (MCCO/) MCCORMICK A A.
PA (TUSE/) TUSE D.
PA (REIN/) REINL S J.
PA (LIND/) LINDBO J A.
PA (TURP/) TURPEN T H.
XX
PI McCormick AA, Tuse D, Reinl SJ, Lindbo JA, Turpen TH;
XX
DR WPI; 2003-492106/46.
DR P-PSDB; ABO23262.
XX
PT Use of a polypeptide self-antigen as a tumor-specific vaccine.
XX
PS Example 2; Page 22; 47pp; English.
XX
CC The invention relates to a polypeptide self-antigen useful as a tumour-
CC specific vaccine in a subject with a tumour or at risk of developing a
CC tumour and is encoded at least in part by a nucleic acid in the cells of
CC the tumour. The polypeptide self antigen is useful for treating or
CC preventing tumour. The present sequence represents DNA encoding a CJ
CC heavy chain variable region linker
XX

SQ Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 72.8%; Score 28.4; DB 8; Length 39;
Best Local Similarity 84.2%; Pred. No. 4.3;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 CTACTGCTACTGGTGCTAGTACTACTGCTGGTGCTAGT 39
Db 2 CTACTGGTGCTAGTACTAGTCTACTGCTGGTGCTAGT 39

Search completed: July 30, 2005, 07:14:49
Job time : 276 secs

RESULT 15
ACD06881
ID ACD06881 standard; DNA; 39 BP.
XX AC ACD06881;
XX DT 06-AUG-2003 (first entry)
XX DE Immunogenic single chain antibody polypeptide (scfv) linker DNA #3.
XX KW Tumour; immunoglobulin variable region; anti-tumour; cytostatic; vaccine;
KW self-antigen; tumour-specific vaccine; B-cell lymphoma-specific vaccine;
KW B-cell lymphoma; single chain antibody polypeptide; scfv; ds.
XX OS Homo sapiens.
XX PN US2003044420-A1.
XX PD 06-MAR-2003.
XX PF 08-FEB-2002; 2002US-00067893.
XX PR 24-SEP-1999; 99US-0155979P.
XX PP 10-MAR-2000; 2000US-00522900.
XX PA (MCCO/) MCCORMICK A A.
PA (TUSE/) TUSE D.
PA (REIN/) REINL S J.
PA (LIND/) LINDBO J A.
PA (TURP/) TURPEN T H.
XX Mccormick AA, Tuse D, Reinl SJ, Lindbo JA, Turpen TH;
WPI; 2003-456552/43.
XX Novel polypeptide self-antigen useful as tumor-specific vaccine in
PT mammals, is produced in plants and mimics one or more epitopes of antigen
PT uniquely expressed by cells of tumor.
XX Example 2; Page 21; 47pp; English.
XX The invention describes a polypeptide self-antigen (I) useful as a tumour
CC -specific vaccine in a subject with a tumour or at risk of developing a
CC tumour, encoded by a nucleic acid (NA) in the cells of the tumour,
CC including an epitope to, or overexpressed by tumour cells; produced in a
CC cell or organism that has been transfected with NA and in a correctly
CC folded form; and capable of inducing an immune response in a mammal. (I)
CC is useful as a tumour-specific vaccine, especially a B-cell lymphoma-
CC specific vaccine. A vaccine is useful for inducing a tumour-specific
CC immune antibody response in a tumour-bearing subject, preferably human or
CC a subject who had a tumour and was treated so that no tumour is
CC clinically or radiographically evident, where the tumour is B-cell
CC lymphoma. This sequence encodes a linker peptide that joins a variable
CC heavy chain region to a variable light chain region to form a single
CC chain antibody polypeptide useful in the tumour-specific vaccine of the
CC invention
XX
SQ Sequence 39 BP; 6 A; 7 C; 13 G; 13 T; 0 U; 0 Other;
Query Match 72.8%; Score 28.4; DB 9; Length 39;
Best Local Similarity 84.2%; Pred. No. 4.3;
Matches 32; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 07:02:14 ; Search time 97 Seconds
(without alignments)
657.884 Million cell updates/sec

Title: US-09-667-237B-12
Perfect score: 39
Sequence: 1 actactgctactggtgtagtagtactactgctggtgtagt 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:*
1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCITUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	27.8	71.3	3376	1 US-08-320-559-29	Sequence 29, Appl
C 2	27.8	71.3	3376	3 US-08-545-860D-29	Sequence 29, Appl
C 3	27.8	71.3	3376	5 PCT-US94-04496-29	Sequence 29, Appl
C 4	26.8	68.7	1534	1 US-07-973-431B-2	Sequence 2, Appli
5	26.4	67.7	1037	4 US-09-181-585-3	Sequence 3, Appli
6	26.4	67.7	1159	4 US-09-181-585-1	Sequence 1, Appli
7	26.4	67.7	1471	4 US-09-181-585-2	Sequence 2, Appli
C 8	26.2	67.2	601	4 US-09-949-016-189405	Sequence 189405,
C 9	26.2	67.2	601	4 US-09-949-016-189406	Sequence 189406,
C 10	26.2	67.2	601	4 US-09-949-016-189407	Sequence 189407,
C 11	26.2	67.2	601	4 US-09-949-016-189408	Sequence 189408,
C 12	26.2	67.2	601	4 US-09-949-016-189409	Sequence 189409,
13	26.2	67.2	825	4 US-09-248-796A-7819	Sequence 7819, Ap
14	26.2	67.2	92074	4 US-09-949-016-17163	Sequence 17163, A
C 15	26.2	67.2	678533	4 US-09-949-016-14577	Sequence 14577, A
C 16	26.2	67.2	678533	4 US-09-949-016-14578	Sequence 14578, A
17	26	66.7	1449	4 US-09-614-221A-468	Sequence 468, App
18	25.2	64.6	939	4 US-09-248-796A-6040	Sequence 6040, Ap
C 19	24.8	63.6	1830	4 US-09-248-796A-409	Sequence 409, App
C 20	24.6	63.1	420	4 US-09-248-796A-1859	Sequence 1859, Ap
C 21	24.6	63.1	517	4 US-09-640-211A-1352	Sequence 1352, Ap
22	24.6	63.1	601	4 US-09-949-016-93964	Sequence 93964, A
23	24.6	63.1	648	4 US-09-248-796A-8852	Sequence 8852, Ap
C 24	24.6	63.1	1188	4 US-09-362-842-5	Sequence 5, Appli
25	24.6	63.1	1671	4 US-09-248-796A-8235	Sequence 8235, Ap
26	24.6	63.1	2289	4 US-09-248-796A-5548	Sequence 5548, Ap
C 27	24.6	63.1	2369	3 US-08-910-925-2	Sequence 2, Appli

C 28	24.6	63.1	2617	4 US-09-949-016-390	Sequence 390, App
C 29	24.6	63.1	9879	4 US-09-949-016-13270	Sequence 13270, A
C 30	24.6	63.1	12921	4 US-09-949-016-14446	Sequence 14446, A
C 31	24.6	63.1	26587	4 US-09-949-016-16636	Sequence 16636, A
32	24.6	63.1	83428	4 US-09-949-016-13610	Sequence 13610, A
33	24.6	63.1	108169	4 US-09-949-016-12898	Sequence 12898, A
34	24.6	63.1	108169	4 US-09-949-016-15907	Sequence 15907, A
C 35	24.6	63.1	140925	4 US-09-949-016-11777	Sequence 11777, A
C 36	24.6	63.1	140982	4 US-09-949-016-16295	Sequence 16295, A
C 37	24.6	63.1	301828	4 US-09-949-016-13969	Sequence 13969, A
38	24.4	62.6	393	4 US-09-248-796A-2714	Sequence 2714, Ap
C 39	24.4	62.6	609	4 US-09-248-796A-3807	Sequence 3807, Ap
40	24.4	62.6	1266	4 US-09-248-796A-314	Sequence 314, App
41	24.2	62.1	246	4 US-09-248-796A-6639	Sequence 6639, Ap
42	24.2	62.1	601	4 US-09-949-016-93963	Sequence 93963, A
43	24.2	62.1	615	4 US-09-248-796A-2859	Sequence 2859, Ap
44	24.2	62.1	711	4 US-09-248-796A-265	Sequence 265, App
45	24.2	62.1	852	4 US-09-248-796A-5507	Sequence 5507, Ap

ALIGNMENTS

RESULT 1
US-08-320-559-29/c
; Sequence 29, Application US/08320559
; Patent No. 5633135
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods for
; TITLE OF INVENTION: Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the
; TITLE OF INVENTION: All-1 Region
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5633135ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/320,559
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/062,443
FILING DATE: 14 MAY 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/971,094
FILING DATE: 30-OCT-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/888,830
FILING DATE: 27-MAY-92
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/805,093
FILING DATE: 11-DEC-91
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-0855
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 3376 base pairs


```
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
US-08-320-559-29

Query Match      71.3%; Score 27.8; DB 1; Length 3376;
Best Local Similarity 82.1%; Pred. No. 1.6;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTACTGCTGGTGTAGT 39
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 765 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 727

RESULT 2
US-08-545-860D-29/c
; Sequence 29, Application US/08545860D
; Patent No. 6040140
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1 Region
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: No. 6040140ris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/545,860D
; FILING DATE: 07-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE: 22-APR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/10930
; FILING DATE: 09-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/327,392
; FILING DATE: 19-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/320,559
; FILING DATE: 11-OCT-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/062,443
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/971,094
; FILING DATE: 30-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/888,839
; FILING DATE: 27-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/805,093
; FILING DATE: 11-DEC-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca Esq., Mark
; REGISTRATION NUMBER: 33,229
```

```
; REFERENCE/DOCKET NUMBER: TJU-1262
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
US-08-545-860D-29

Query Match      71.3%; Score 27.8; DB 3; Length 3376;
Best Local Similarity 82.1%; Pred. No. 1.6;
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTACTGCTGGTGTAGT 39
   ||||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 765 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 727

RESULT 3
PCT-US94-04496-29/c
; Sequence 29, Application PC/TUS9404496
; GENERAL INFORMATION:
; APPLICANT: Croce, Carlo
; APPLICANT: Canaani, Eli
; TITLE OF INVENTION: Diagnostics, Therapeutics and Methods
; TITLE OF INVENTION: for Detection and Treatment of Acute Leukemias
; TITLE OF INVENTION: Resulting from Chromosome Abnormalities in the All-1
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock, Washburn, Kurtz, Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/04496
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: DeLuca Esq., Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1242
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3376 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 196..1902
PCT-US94-04496-29

Query Match      71.3%; Score 27.8; DB 5; Length 3376;
Best Local Similarity 82.1%; Pred. No. 1.6;
```



```
Matches 32; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGTAGT 39
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 765 ACTACTGCTGCTGCTGCTGCTACTGCTGCTGCTACT 727
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 4
US-07-973-431B-2/c
; Sequence 2, Application US/07973431B
; Patent No. 5652144
; GENERAL INFORMATION:
; APPLICANT: Lu, Yinchen
; APPLICANT: Haseltine, William A
; TITLE OF INVENTION: YC1 Protein, Gene, And Uses Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David G. Conlin; Dike, Bronstein,
; ADDRESSEE: Roberts & Cushman
; STREET: 130 Water Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,431B
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Eisenstein, Ronald I
; REGISTRATION NUMBER: 30628
; REFERENCE/DOCKET NUMBER: 41968
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 523-3400
; TELEFAX: (617) 523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1534 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
US-07-973-431B-2

Query Match 68.7%; Score 26.8; DB 1; Length 1534;
Best Local Similarity 81.6%; Pred. No. 3.1;
Matches 31; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGTAG 38
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 221 ACTGCTGCTACTGTTGTTATTACTGCTGGTGTGG 184
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 5
US-09-181-585-3
; Sequence 3, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 11000900101
; CURRENT APPLICATION NUMBER: US/09/181,585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1037
```

```
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
; OTHER INFORMATION: comprising exons E, C, and A
US-09-181-585-3

Query Match 67.7%; Score 26.4; DB 4; Length 1037;
Best Local Similarity 83.3%; Pred. No. 4;
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTGCTAGTACTACTGCTGGTGTCT 36
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 667 ACTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGT 702
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 6
US-09-181-585-1
; Sequence 1, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 11000900101
; CURRENT APPLICATION NUMBER: US/09/181,585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1159
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-181-585-1

Query Match 67.7%; Score 26.4; DB 4; Length 1159;
Best Local Similarity 83.3%; Pred. No. 4.1;
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTGCTAGTACTACTGCTGGTGTCT 36
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 479 ACTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGT 514
    ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 7
US-09-181-585-2
; Sequence 2, Application US/09181585
; Patent No. 6524791
; GENERAL INFORMATION:
; APPLICANT: Ranum, Laura P.W.
; APPLICANT: Koob, Michael
; TITLE OF INVENTION: SPINOCEREBELLAR ATAXIA TYPE 8 AND METHODS OF DETECTION
; FILE REFERENCE: 11000900101
; CURRENT APPLICATION NUMBER: US/09/181,585
; CURRENT FILING DATE: 1998-10-28
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 1471
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: cDNA
; OTHER INFORMATION: comprising exons D, C, B, and A
US-09-181-585-2

Query Match 67.7%; Score 26.4; DB 4; Length 1471;
Best Local Similarity 83.3%; Pred. No. 4.2;
Matches 30; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGCTGCTAGTACTACTGCTGGTGTCT 36
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1101 ACTACTGCTACTGCTGCTGCTGCTGCTGCTGCTGT 1136
    ||||| ||||| ||||| ||||| ||||| ||||| |||||
```



```

RESULT 8
US-09-949-016-189405/c
; Sequence 189405, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189405
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-189405

```

```
Query Match      67.2%; Score 26.2; DB 4; Length 601;
Best Local Similarity 79.5%; Pred. No. 4.4;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
```

1 ACTACTGCTACTGGTCTAGTACTACTGCTGGTCTAGT 39
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 135 ACTACTACTATTGCTACTACTACTACTACTGCTACT 97
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 9
US-09-949-016-189406/c
; Sequence 189406, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189406
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-189406

```

Query Match 67.2%; Score 26.2; DB 4; Length 601;
Best Local Similarity 79.5%; Pred. No. 4.4;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy 1 ACTACTGCTACTGGTGTCTAGTACTGCTGGTGCTAGT 39
 ||||| ||||| ||||| ||||| ||||| ||||| |||||
p6 209 ACTACTACTATTGCTACTACTACTGCTACTACT 171

RESULT 10
US-09-949-016-189407/c
; Sequence 189407, Application US/09949016

```

; Patent No. 6812339
;
; GENERAL INFORMATION:
;
; APPLICANT: VENTER, J. Craig et al.
;
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;
; FILE REFERENCE: CL001307
;
; CURRENT APPLICATION NUMBER: US/09/949,016
;
; CURRENT FILING DATE: 2000-04-14
;
; PRIOR APPLICATION NUMBER: 60/241,755
;
; PRIOR FILING DATE: 2000-10-20
;
; PRIOR APPLICATION NUMBER: 60/237,768
;
; PRIOR FILING DATE: 2000-10-03
;
; PRIOR APPLICATION NUMBER: 60/231,498
;
; PRIOR FILING DATE: 2000-09-08
;
; NUMBER OF SEQ ID NOS: 207012
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 189407
;
; LENGTH: 601
;
; TYPE: DNA
;
; ORGANISM: Human
;
; US-09-949-016-189407

```

Query Match 67.2%; Score 26.2; DB 4; Length 601;
Best Local Similarity 79.5%; Pred. No. 4.4;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Caps 0;

Qy

1 ACTACTGCTACTGGTGTCTAGTACTACTGCTGGTGTAGT 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

p6

244 ACTACTACTACTATTGCTACTACTACTACTCTGCTACTACT 206

```

RESULT 11
US-09-949-016-189408/c
; Sequence 189408, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189408
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-189408

```

Query Match 67.2%; Score 26.2; DB 4; Length 601;
Best Local Similarity 79.5%; Pred. No. 4.4;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

Qy

1 ACTACTGCTACTGGTGTCTAGTACTACTGCTGGTGCTAGT 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

p6

259 ACTACTACTATTGCTACTACTACTACTGCTACTACT 221

RESULT 12
US-09-949-016-189409/c
; Sequence 189409, Application US/099494016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNI
; TITLE OF INVENTION: WITH HUMAN DISEASE

; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 189409
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-189409

Query Match 67.2%; Score 26.2; DB 4; Length 601;
Best Local Similarity 79.5%; Pred. No. 4.4;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGGTGCTAGT 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 397 ACTACTACTATTGCTACTACTACTACTGCTACTACT 359

RESULT 13
US-09-248-796A-7819
; Sequence 7819, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 7819
; LENGTH: 825
; TYPE: DNA
; ORGANISM: Candida albicans
US-09-248-796A-7819

Query Match 67.2%; Score 26.2; DB 4; Length 825;
Best Local Similarity 79.5%; Pred. No. 4.6;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGGTGCTAGT 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 ACTACTGCTACTGCTACTACTGCTACTGCTACTGCTACT 459

RESULT 14
US-09-949-016-17163
; Sequence 17163, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17163
; LENGTH: 92074
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17163

Query Match 67.2%; Score 26.2; DB 4; Length 92074;
Best Local Similarity 79.5%; Pred. No. 9;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGGTGCTAGT 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40991 ACTACTACTATTGCTACTACTACTACTGCTACTACT 41029

RESULT 15
US-09-949-016-14577/c
; Sequence 14577, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 14577
; LENGTH: 678533
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(678533)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14577

Query Match 67.2%; Score 26.2; DB 4; Length 678533;
Best Local Similarity 79.5%; Pred. No. 12;
Matches 31; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGGTGCTAGT 39
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 216377 ACTACTACTACTACTACTACTACTACTACTGCTAGT 216339

Search completed: July 30, 2005, 08:17:06
Job time : 101 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 07:10:14 ; Search time 412 Seconds
(without alignments)
612.675 Million cell updates/sec

Title: US-09-667-237B-12
Perfect score: 39
Sequence: 1 actactgctactggtgtagtactactgctggtgtagt 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*

21: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

23: /cgn2_6/ptodata/1/pubpna/US11A_PUBCOMB.seq:*

24: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

25: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*

26: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	100.0	39	10	US-09-539-382-45 Sequence 45, Appl
2	39	100.0	39	14	US-10-067-790-45 Sequence 45, Appl
3	39	100.0	39	14	US-10-067-892-45 Sequence 45, Appl
4	39	100.0	39	14	US-10-067-893-45 Sequence 45, Appl
5	30	76.9	109453	19	US-10-388-838-81 Sequence 81, Appl
C 6	29.4	75.4	192	19	US-10-674-124A-10191 Sequence 10191, A
C 7	29	74.4	201	20	US-10-719-993-1896 Sequence 1896, Ap

C 8	29	74.4	201	20	US-10-719-993-1903	Sequence 1903, Ap
C 9	29	74.4	201	20	US-10-719-993-1907	Sequence 1907, Ap
C 10	29	74.4	201	20	US-10-719-993-10972	Sequence 10972, A
C 11	29	74.4	2059	17	US-10-442-017-16	Sequence 16, Appl
C 12	29	74.4	3179	20	US-10-719-993-97	Sequence 97, Appl
C 13	29	74.4	3261	20	US-10-719-993-95	Sequence 95, Appl
C 14	29	74.4	3637	20	US-10-719-993-96	Sequence 96, Appl
C 15	29	74.4	289730	20	US-10-719-993-6780	Sequence 6780, Ap
C 16	28.4	72.8	39	10	US-09-539-382-49	Sequence 49, Appl
C 17	28.4	72.8	39	14	US-10-067-790-49	Sequence 49, Appl
C 18	28.4	72.8	39	14	US-10-067-892-49	Sequence 49, Appl
C 19	28.4	72.8	39	14	US-10-067-893-49	Sequence 49, Appl
C 20	27.8	71.3	201	20	US-10-719-993-1895	Sequence 1895, Ap
C 21	27.8	71.3	201	20	US-10-719-993-1902	Sequence 1902, Ap
C 22	27.8	71.3	201	20	US-10-719-993-1906	Sequence 1906, Ap
C 23	27.8	71.3	201	20	US-10-719-993-10948	Sequence 10948, A
C 24	27.8	71.3	488	10	US-09-918-995-19918	Sequence 19918, A
C 25	27.8	71.3	495	21	US-10-800-322-55	Sequence 55, Appl
C 26	27.8	71.3	544	16	US-10-029-386-22806	Sequence 22806, A
C 27	27.8	71.3	553	9	US-09-920-300A-1461	Sequence 1461, Ap
C 28	27.8	71.3	553	13	US-10-033-528-1461	Sequence 1461, Ap
C 29	27.8	71.3	553	16	US-10-099-926-1461	Sequence 1461, Ap
C 30	27.8	71.3	553	22	US-10-961-527-1461	Sequence 1461, Ap
C 31	27.8	71.3	586	16	US-10-029-386-9094	Sequence 9094, Ap
C 32	27	69.2	2510	17	US-10-172-118-1031	Sequence 1031, Ap
C 33	27	69.2	2510	18	US-10-342-887-1031	Sequence 1031, Ap
C 34	27	69.2	3277	20	US-10-723-860-463	Sequence 463, App
C 35	26.8	68.7	60	10	US-09-539-382-55	Sequence 55, Appl
C 36	26.8	68.7	60	14	US-10-067-790-55	Sequence 55, Appl
C 37	26.8	68.7	60	14	US-10-067-892-55	Sequence 55, Appl
C 38	26.8	68.7	60	14	US-10-067-893-55	Sequence 55, Appl
C 39	26.8	68.7	1369	19	US-10-322-281-28	Sequence 28, Appl
C 40	26.8	68.7	1500	16	US-10-269-909-67	Sequence 67, Appl
C 41	26.8	68.7	1509	14	US-10-175-523-40	Sequence 40, Appl
C 42	26.8	68.7	1536	21	US-10-965-898-90	Sequence 90, Appl
C 43	26.8	68.7	1679	17	US-10-172-118-1675	Sequence 1675, Ap
C 44	26.8	68.7	1679	18	US-10-342-887-1675	Sequence 1675, Ap
C 45	26.8	68.7	88232	13	US-10-087-192-1699	Sequence 1699, Ap

ALIGNMENTS

RESULT 1
US-09-539-382-45
; Sequence 45, Application US/09539382
; Publication No. US2003004417A1
; GENERAL INFORMATION:
; APPLICANT: MCCORMICK, Alison
; APPLICANT: TUSE, Daniel
; APPLICANT: REINL, Stephen
; APPLICANT: LINDBO, John
; APPLICANT: TURPEN, Thomas
; TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CAN
; FILE REFERENCE: 18696-169195
; CURRENT APPLICATION NUMBER: US/09/539,382
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 60/155,579
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..(?)
; OTHER INFORMATION: linker
US-09-539-382-45

Query Match 100.0%; Score 39; DB 10; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39

RESULT 2
US-10-067-790-45
; Sequence 45, Application US/10067790
; Publication No. US20030035807A1
; GENERAL INFORMATION:
; APPLICANT: MCCORMICK, Alison
; APPLICANT: TUSE, Daniel
; APPLICANT: REINL, Stephen
; APPLICANT: LINDBO, John
; APPLICANT: TURPEN, Thomas
; TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CAN
; FILE REFERENCE: 18696-169194
; CURRENT APPLICATION NUMBER: US/10/067,790
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/522,900
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 60/155,579
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()

US-10-067-790-45
Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39

RESULT 3
US-10-067-892-45
; Sequence 45, Application US/10067892
; Publication No. US20030039659A1
; GENERAL INFORMATION:
; APPLICANT: MCCORMICK, Alison
; APPLICANT: TUSE, Daniel
; APPLICANT: REINL, Stephen
; APPLICANT: LINDBO, John
; APPLICANT: TURPEN, Thomas
; TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS
; FILE REFERENCE: 18696-169194
; CURRENT APPLICATION NUMBER: US/10/067,892
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US/09/522,900
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()

US-10-067-892-45
Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39

RESULT 4
US-10-067-893-45
; Sequence 45, Application US/10067893
; Publication No. US2003004420A1
; GENERAL INFORMATION:
; APPLICANT: MCCORMICK, Alison
; APPLICANT: TUSE, Daniel
; APPLICANT: REINL, Stephen
; APPLICANT: LINDBO, John
; APPLICANT: TURPEN, Thomas
; TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CAN
; FILE REFERENCE: 18696-169194
; CURRENT APPLICATION NUMBER: US/10/067,893
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 09/522,900
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 60/155,579
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()

US-10-067-893-45
Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39

RESULT 5
US-10-388-838-81
; Sequence 81, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388,838
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 109453
; TYPE: DNA
; ORGANISM: Mus musculus

US-10-388-838-81
Query Match 76.9%; Score 30; DB 19; Length 109453;
Best Local Similarity 86.8%; Pred. No. 1.4;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

US-10-067-892-45
Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39

RESULT 4
US-10-067-893-45
; Sequence 45, Application US/10067893
; Publication No. US2003004420A1
; GENERAL INFORMATION:
; APPLICANT: MCCORMICK, Alison
; APPLICANT: TUSE, Daniel
; APPLICANT: REINL, Stephen
; APPLICANT: LINDBO, John
; APPLICANT: TURPEN, Thomas
; TITLE OF INVENTION: SELF ANTIGEN VACCINES FOR TREATING B CELL LYMPHOMAS AND OTHER CAN
; FILE REFERENCE: 18696-169194
; CURRENT APPLICATION NUMBER: US/10/067,893
; CURRENT FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: 09/522,900
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: US 60/155,579
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 45
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: ()..()

US-10-067-893-45
Query Match 100.0%; Score 39; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
|||||
Db 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39

RESULT 5
US-10-388-838-81
; Sequence 81, Application US/10388838
; Publication No. US20040180344A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; APPLICANT: Marc Malandro
; TITLE OF INVENTION: Novel Therapeutic Targets in Cancer
; FILE REFERENCE: 529452001600
; CURRENT APPLICATION NUMBER: US/10/388,838
; CURRENT FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 114
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 109453
; TYPE: DNA
; ORGANISM: Mus musculus

US-10-388-838-81
Query Match 76.9%; Score 30; DB 19; Length 109453;
Best Local Similarity 86.8%; Pred. No. 1.4;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Oy 2 CTACTGCTACTGGTGTAGTAGTACTACTGCTGCTGGTGCTAGT 39
Db 22948 CTGCTGCTGCTGGTGTAGTAGTATTCCTGCTGGTGCTAGT 22985

RESULT 6
US-10-674-124A-10191/c
; Sequence 10191, Application US/10674124A
; Publication No. US20040197797A1
; GENERAL INFORMATION:
; APPLICANT: INOKO, Hidetoshi
; APPLICANT: TAMIYA, Gen
; TITLE OF INVENTION: GENE MAPPING METHOD USING MICROSATELLITE
; TITLE OF INVENTION: GENETIC POLYMORPHISM MARKERS
; FILE REFERENCE: ORIN-003CIP
; CURRENT APPLICATION NUMBER: US/10/674,124A
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 10/257,511
; PRIOR FILING DATE: 2003-03-07
; PRIOR APPLICATION NUMBER: PCT/JP00/07621
; PRIOR FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: JP2000-112699
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: JP2002-327516
; PRIOR FILING DATE: 2002-09-28
; PRIOR APPLICATION NUMBER: JP2002-383869
; PRIOR FILING DATE: 2002-12-09
; NUMBER OF SEQ ID NOS: 27110
; SEQ ID NO 10191
; LENGTH: 192
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: DIS07_10002156
; OTHER INFORMATION: Located on chromosome 6
; FEATURE:
; OTHER INFORMATION: Distance between a terminus base of telomere on
; OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base
; OTHER INFORMATION: sequence : 51933016
; FEATURE:
; OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of
; OTHER INFORMATION: sequence listing upward to telomere on chromosomal short arm and
; OTHER INFORMATION: 5'-terminus of this base sequence : 140955
US-10-674-124A-10191

Query Match 75.4%; Score 29.4; DB 19; Length 192;
Best Local Similarity 84.6%; Pred. No. 0.8;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ACTACTGCTACTGGTGTAGTAGTACTACTGCTGCTGGTGCTAGT 39
Db 132 ACTACTACTGCTGCTGCTACTACTACTACTGCTGCTGCTATT 94

RESULT 7
US-10-719-993-1896/c
; Sequence 1896, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1896
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-1896

Query Match 74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ACTACTGCTACTGGTGTAGTAGTACTACTGCTGCTGGTGCTAGT 39
Db 122 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 84

RESULT 8
US-10-719-993-1903/c
; Sequence 1903, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1903
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-1903

Query Match 74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ACTACTGCTACTGGTGTAGTAGTACTACTGCTGCTGGTGCTAGT 39
Db 122 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 84

RESULT 9
US-10-719-993-1907/c
; Sequence 1907, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1907
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-1907

Query Match 74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy 1 ACTACTGCTACTGGTGTAGTAGTACTACTGCTGCTGGTGCTAGT 39
Db 122 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 84

RESULT 10
US-10-719-993-10972/c
; Sequence 10972, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH


```

; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10972
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-10972

Query Match      74.4%; Score 29; DB 20; Length 201;
Best Local Similarity 82.1%; Pred. No. 1.1;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 84

RESULT 11
US-10-442-017-16/c
; Sequence 16, Application US/10442017
; Publication No. US20030215950A1
; GENERAL INFORMATION:
; APPLICANT: Battelle Memorial Institute
; APPLICANT: Lasure, Linda L.
; APPLICANT: Dai, Ziyu
; TITLE OF INVENTION: Isolated Polynucleotides and Methods of Promoting a Morphology In
; TITLE OF INVENTION: a Fungus
; FILE REFERENCE: BA4-195
; CURRENT APPLICATION NUMBER: US/10/442,017
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60\382,132
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 2059
; TYPE: DNA
; ORGANISM: Aspergillus niger
US-10-442-017-16

Query Match      74.4%; Score 29; DB 17; Length 2059;
Best Local Similarity 86.5%; Pred. No. 1.6;
Matches 32; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 TACTGCTACTGGTGTAGTACTACTGCTGCTGGTGCTAGT 39
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1396 TGCTGCTGCTAGTGTAGTGTAGTGTGCTGCTAGT 1360

RESULT 12
US-10-719-993-97/c
; Sequence 97, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 3179
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-97

Query Match      74.4%; Score 29; DB 20; Length 3179;

```

```

Best Local Similarity 82.1%; Pred. No. 1.7;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 863 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 825

RESULT 13
US-10-719-993-95/c
; Sequence 95, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 3261
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-95

Query Match      74.4%; Score 29; DB 20; Length 3261;
Best Local Similarity 82.1%; Pred. No. 1.7;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 863 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 825

RESULT 14
US-10-719-993-96/c
; Sequence 96, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3637
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-719-993-96

Query Match      74.4%; Score 29; DB 20; Length 3637;
Best Local Similarity 82.1%; Pred. No. 1.8;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGCTAGT 39
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 863 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 825

RESULT 15
US-10-719-993-6780/c
; Sequence 6780, Application US/10719993
; Publication No. US20040265849A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001496

```



```
; CURRENT APPLICATION NUMBER: US/10/719,993
; CURRENT FILING DATE: 2003-11-24
; NUMBER OF SEQ ID NOS: 55342
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6780
; LENGTH: 289730
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(289730)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-
US-10-719-993-6780

Query Match      74.4%; Score 29; DB 20; Length 289730;
Best Local Similarity 82.1%; Pred. No. 3.6;
Matches 32; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 ACTACTGCTACTGCTGCTAGTAGTACTACTGCTGCTGCTAGT 39
      ||||||| ||| |||| |:||||| |||||
Db      214259 ACTACTGCTGCTGCTGCTGCTGCTGCTGCTGCTACT 214221
```

Search completed: July 30, 2005, 08:24:04
Job time : 416 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 06:59:54 ; Search time 2067 Seconds
(without alignments)
718.194 Million cell updates/sec

Title: US-09-667-237B-12
Perfect score: 39
Sequence: 1 actactgtactggtgtagtagtactactgctggtgtagt 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_htc: *
4: gb_est3: *
5: gb_est4: *
6: gb_est5: *
7: gb_est6: *
8: gb_gss1: *
9: gb_gss2: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	33.8	86.7	410	FR0021942	AL014813 F.rubripe
2	31	79.5	513	BZ423698	BZ423698 id52c10.g
3	31	79.5	619	FR0006944	Z90754 F.rubripes
C 4	30.6	78.5	280	FR0019522	AL012412 F.rubripe
C 5	30	76.9	152	FR0013693	AL004939 F.rubripe
6	30	76.9	480	BZ643398	BZ643398 OGAOW57TC
C 7	30	76.9	493	AL931932	AL931932 AL931932
C 8	30	76.9	843	BZ643413	BZ643413 OGAOW57TM
C 9	29.4	75.4	207	FR0021848	AL014719 F.rubripe
10	29.4	75.4	257	FR0026883	AL019712 F.rubripe
C 11	29.4	75.4	307	BZ683794	BZ683794 PUBCV45TD
C 12	29.4	75.4	470	FR0018463	AL011359 F.rubripe
13	29.4	75.4	472	AQ934726	AQ934726 RPCI-23-2
14	29.4	75.4	526	CNS03CM0	AL237969 Tetraodon
C 15	29.4	75.4	735	CNS04NSM	AL299119 Tetraodon
16	29.4	75.4	764	CG290979	CG290979 OGXFM44TH
17	29.4	75.4	951	CNS0414A	AL269731 Tetraodon
C 18	29	74.4	940	AZ205951	AZ205951 SP_0088_A
C 19	28.6	73.3	425	CNS01XJ9	AL171774 Tetraodon
C 20	28.6	73.3	469	CL569187	CL569187 4-12-4 Ma
C 21	28.6	73.3	610	FR0047551	AL444336 Fugu rubr
C 22	28.4	72.8	262	CE385582	CE385582 tigr-gss-
C 23	28.4	72.8	452	BE679837	BE679837 df57a05.y
24	28.4	72.8	477	FR0026865	AL019694 F.rubripe

C 25	28.4	72.8	500	5	BP190034	BP190034
26	28.4	72.8	567	9	FR0006951	Z90761 F.rubripes
C 27	28.4	72.8	619	9	FR0047423	AL444208 Fugu rubr
C 28	28.4	72.8	661	4	BJ661564	BJ661564 BJ661564
29	28.4	72.8	676	4	BJ649626	BJ649626 BJ649626
30	28.4	72.8	805	9	CNS04RW2	AL304427 Tetraodon
31	28.4	72.8	818	9	CL843342	CL843342 OR_CBA007
32	28.4	72.8	905	9	CL288114	CL288114 ZMMBBb063
33	28.4	72.8	939	9	CG900918	CG900918 ZMMBBb051
34	28.4	72.8	993	8	AQ687985	AQ687985 nbxb0076B
C 35	28	71.8	168	8	BH784725	BH784725 fzbmb013f0
C 36	28	71.8	267	9	CE589218	CE589218 tigr-gss-
C 37	28	71.8	388	9	FR0019523	AL012413 F.rubripe
38	28	71.8	548	7	CN251992	CN251992 EST017923
C 39	28	71.8	562	5	BUI26074	BUI26074 603151355
C 40	28	71.8	580	8	BH763893	BH763893 BMBAC314F
C 41	28	71.8	659	4	BM627819	BM627819 170006874
C 42	28	71.8	684	2	BF612474	BF612474 daal8el0.
C 43	28	71.8	687	5	BUI26727	BUI26727 603150929
C 44	28	71.8	689	5	BUI26090	BUI26090 603150342
C 45	28	71.8	690	2	BF612625	BF612625 daal9h03.

ALIGNMENTS

RESULT 1
FR0021942/c

LOCUS FR0021942 410 bp DNA linear GSS 25-FEB-2004
DEFINITION F.rubripes GSS sequence, clone 070F18aB11, genomic survey sequence.
ACCESSION AL014813
VERSION AL014813.1 GI:2681181
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes (Fugu rubripes)
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Takifugu.

REFERENCE 1

AUTHORS Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
Bouchireb,N., Cottage,A., Yeo,G.S., Umrانيا,Y., Williams,G. and
Brenner,S.

TITLE Generation and analysis of 25 Mb of genomic DNA from the pufferfish

Fugu rubripes by sequence scanning

Genome Res. 9 (10), 960-971 (1999)

MEDLINE 99455097

PUBMED 10523524

REFERENCE 2 (bases 1 to 410)

AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
Williams,G. and Brenner,S.

TITLE Direct Submission

JOURNAL Submitted (08-DEC-1997) MRC Human Genome Mapping Project Resource

Centre Hinxtion, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk

COMMENT Vector: pBluescript II KS

V type: phagemid

PRIMER: KS

DESCR: One pass dye-terminator sequencing of cosmid cloned genomic

sequence.

FEATURES

source

1. 410

/organism="Takifugu rubripes"

/mol_type="genomic DNA"

/db_xref="taxon:31033"

/clone="070F18aB11"

/clone_lib="cosmid 070F18"

ORIGIN

Query Match 86.7%; Score 33.8; DB 9; Length 410;
Best Local Similarity 89.7%; Pred. No. 0.078;
Matches 35; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

One pass dye-terminator sequencing of cosmid cloned genomic sequence.

FEATURES
source Location/Qualifiers
1. .280
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="031C10af9"
/clone_lib="cosmid 031C10"

ORIGIN
Query Match 78.5%; Score 30.6; DB 9; Length 280;
Best Local Similarity 84.6%; Pred. No. 1.1;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGCTGGTCTAGT 39
|||||
Db 226 ACTGCTGCTACTGTTGCTACTACTGCTGCTGNTGNTAGT 188
|||||

RESULT 5
FR0013693/c
LOCUS FR0013693 152 bp DNA linear GSS 25-FEB-2004
DEFINITION F.rubripes GSS sequence, clone 133B16cd1, genomic survey sequence.
ACCESSION AL004939
VERSION AL004939.1 GI:2450509
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes (Fugu rubripes)
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Takifugu.

REFERENCE 1
-AUTHORS Elgar,G., Clark,M.S., Meek,S., Smith,S., Warner,S., Edwards,Y.J.,
Bouchireb,N., Cottage,A., Yeo,G.S., Umrانيا,Y., Williams,G. and
Brenner,S.
Generation and analysis of 25 Mb of genomic DNA from the pufferfish
Fugu rubripes by sequence scanning
Genome Res. 9 (10), 960-971 (1999)
99455097
MEDLINE 10523524
-PUBMED 2 (bases 1 to 152)
AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrانيا,Y.,
Williams,G. and Brenner,S.
Direct Submission
TITLE Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
JOURNAL Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgmp.mrc.ac.uk
COMMENT Vector: pBluescript II KS
V type: phagemid
PRIMER: KS
DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
sequence.

FEATURES
source Location/Qualifiers
1. .152
/organism="Takifugu rubripes"
/mol_type="genomic DNA"
/db_xref="taxon:31033"
/clone="133B16cd1"
/clone_lib="cosmid 133B16"

ORIGIN
Query Match 76.9%; Score 30; DB 9; Length 152;
Best Local Similarity 84.6%; Pred. No. 1.7;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 ACTACTGCTACTGGTCTAGTACTACTGCTGCTGGTCTAGT 39
|||||
Db 90 ACTGCTACTACTGCTGCTGGTACTACTGCTGCTGCTANT 52
|||||

RESULT 6

BZ643398
LOCUS BZ643398 480 bp DNA linear GSS 29-JAN-2003
DEFINITION OGAOW57TC ZM_0.7_1.5_KB Zea mays genomic clone ZMMBma0111J17,
genomic survey sequence.
ACCESSION BZ643398
VERSION BZ643398.1 GI:28104877
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 480)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Nunberg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
JOURNAL Other GSSs: OGAOW57TM
COMMENT Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
FEATURES
source Location/Qualifiers
1. .480
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBma0111J17"
/clone_lib="ZM_0.7_1.5_KB"
/note="Vector: pBCSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN
Query Match 76.9%; Score 30; DB 8; Length 480;
Best Local Similarity 86.8%; Pred. No. 1.8;
Matches 33; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 CTACTGCTACTGGTCTAGTACTACTGCTGCTGGTCTAGT 39
|||||
Db 63 CTACTGCTACTGCTACTACTACTACTGCTGCTGCTACT 100
|||||

RESULT 7
AL931932/c
LOCUS AL931932 493 bp mRNA linear EST 14-NOV-2002
DEFINITION AL931932 NAP1 Anopheles gambiae cDNA clone NAP1-P87-E-03-5, mRNA
sequence.
ACCESSION AL931932
VERSION AL931932.1 GI:24973912
KEYWORDS EST.
SOURCE Anopheles gambiae (African malaria mosquito)
ORGANISM Anopheles gambiae
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
Anopheles.
REFERENCE 1 (bases 1 to 493)
AUTHORS Christophides,G.K., Blass,K., Zdobnov,E.M., Carmouche,R., Benes,V.
and Kafatos,F.C.
TITLE Anopheles gambiae EST, European Molecular Biology Laboratory
JOURNAL Unpublished (2002)
COMMENT Contact: Christophides GK
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerohofstrasse 1, 69117 Heidelberg, Germany
Tel: +49 6221 387-440
Fax: +49 6221 387-306
Email: christop@embl-heidelberg.de

MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 735)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
FEATURES Location/Qualifiers
 1..735
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone="123M05"
 /clone_lib="G"
 /note="Genoscope sequence ID : COBG123AG03LP1~end : T7"
ORIGIN
Query Match 75.4%; Score 29.4; DB 9; Length 735;
Best Local Similarity 84.6%; Pred. No. 3.1;
Matches 33; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 ACTACTGCTACTGGTGTAGTACTACTGCTGGTGTAGT 39
 ||||| ||||| ||||| ||||| ||||| |||||
Db 451 ACTACTACTACTGCTACTGCTACTACTGCTGCTGCTACT 413

Search completed: July 30, 2005, 08:15:25
Job time : 2074 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 30, 2005, 06:23:19 ; Search time 1555 Seconds
(without alignments)
1215.276 Million cell updates/sec

Title: US-09-667-237B-12
Perfect score: 39
Sequence: 1 actactgctactggtgtagtagtactactgctggtgtagt 39

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues 9416466
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:

- 1: gb_ba:*
- 2: gb_htg:*
- 3: gb_in:*
- 4: gb_om:*
- 5: gb_ov:*
- 6: gb_pat:*
- 7: gb_ph:*
- 8: gb_pl:*
- 9: gb_pr:*
- 10: gb_ro:*
- 11: gb_sts:*
- 12: gb_sy:*
- 13: gb_un:*
- 14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	39	100.0	39	6	AX250377	AX250377 Sequence
2	37	94.9	38	6	AX108708	AX108708 Sequence
C 3	31.6	81.0	40346	2	AP006490_7	Continuation (8 of
C 4	31.6	81.0	110000	2	AP006490_6	Continuation (7 of
C 5	31	79.5	171710	5	BX004814	BX004814 Zebrafish
C 6	31	79.5	218404	5	BX470087	BX470087 Zebrafish
C 7	31	79.5	241173	2	AC126150	AC126150 Rattus no
8	30	76.9	402	11	BV090840	BV090840 RPAMSEQO
9	30	76.9	410	3	AF329581	AF329581 Plasmodiu
10	30	76.9	558	3	AY375168	AY375168 Plasmodiu
11	30	76.9	5460	10	AY004216	AY004216 Mus muscu
12	30	76.9	109453	6	CQ869892	CQ869892 Sequence
C 13	30	76.9	203739	2	AC117361	AC117361 Rattus no
14	30	76.9	241381	10	AC087063	AC087063 Mus muscu
15	30	76.9	255613	2	AC117014	AC117014 Rattus no
C 16	29.6	75.9	79531	9	AL390037	AL390037 Human DNA
17	29.4	75.4	420	5	SAU418697	AJ418697 Sparus au
18	29.4	75.4	533	3	AB116615	AB116615 Plasmodiu
C 19	29.4	75.4	543	8	AF413050S1	AF413050 Zea mays

C 20	29.4	75.4	600	8	AY588386	AY588386 Humulus l
21	29.4	75.4	22398	5	FRU271723	AJ271723 Fugu rubr
C 22	29.4	75.4	70833	2	AC134512	AC134512 Rattus no
C 23	29.4	75.4	74586	9	HSJ281E18	AL109982 Human DNA
24	29.4	75.4	143099	2	AC009926	AC009926 Homo sapi
C 25	29.4	75.4	146907	2	AC141031	AC141031 Rattus no
26	29.4	75.4	167198	2	AC148509	AC148509 Macropus
27	29.4	75.4	171427	10	AC126695	AC126695 Mus muscu
C 28	29.4	75.4	188741	2	AC146995	AC146995 Arbacia p
29	29.4	75.4	205025	2	AC121681	AC121681 Rattus no
30	29.4	75.4	209387	2	AC096448	AC096448 Rattus no
C 31	29.4	75.4	217325	2	AC121428	AC121428 Rattus no
C 32	29.4	75.4	221083	10	AC103597	AC103597 Mus muscu
33	29.4	75.4	224364	2	AC094468	AC094468 Rattus no
C 34	29.4	75.4	240155	2	AC129826	AC129826 Rattus no
C 35	29.4	75.4	241943	2	AC107476	AC107476 Rattus no
36	29.4	75.4	244903	2	AC097807	AC097807 Rattus no
C 37	29.4	75.4	251830	2	AC095714	AC095714 Rattus no
38	29.4	75.4	255665	2	AC123012	AC123012 Rattus no
C 39	29	74.4	3438	6	AX151593	AX151593 Sequence
40	29	74.4	147367	2	AC073966	AC073966 Homo sapi
41	29	74.4	153304	9	AC092155	AC092155 Homo sapi
C 42	29	74.4	223793	2	AC023942	AC023942 Homo sapi
C 43	29	74.4	292967	14	AF369029	AF369029 White spo
C 44	29	74.4	305107	6	AX151396	AX151396 Sequence
C 45	29	74.4	305107	14	AF332093	AF332093 White spo

ALIGNMENTS

RESULT 1	AX250377	AX250377	Sequence 45 from Patent WO0168682.	39 bp	DNA	linear	PAT 05-OCT-2001
LOCUS	AX250377	AX250377					
DEFINITION	AX250377	AX250377					
ACCESSION	AX250377	AX250377					
VERSION	AX250377.1	GI:15984141					
KEYWORDS							
SOURCE		unidentified					
ORGANISM		unidentified					
		unclassified.					
REFERENCE	1						
AUTHORS		Reinl,S.J. and Turpen,T.H.					
TITLE		Self antigen vaccines for treating b cell lymphomas and other cancers					
JOURNAL		Patent: WO 0168682-A 45 20-SEP-2001;					
		Large Scale Biology Corporation (US)					
FEATURES		Location/Qualifiers					
source		1. .39					
		/organism="unidentified"					
		/mol_type="unassigned DNA"					
		/db_xref="taxon:32644"					
		/note="linker"					

ORIGIN

Query Match	100.0%;	Score 39;	DB 6;	Length 39;
Best Local Similarity	100.0%;	Pred. No. 0.0068;		
Matches	39;	Conservative	0;	Mismatches 0;
		Indels	0;	Gaps 0;
QY	1	ACTACTGCTACTGCTAGTACTACTGCTGCTAGT	39	
Db	1	ACTACTGCTACTGCTAGTACTACTGCTGCTAGT	39	
RESULT 2	AX108708	AX108708	Sequence 12 from Patent WO0123543.	38 bp
LOCUS	AX108708	AX108708		DNA
DEFINITION	AX108708	AX108708		linear
ACCESSION	AX108708	AX108708		PAT 30-APR-2001
VERSION	AX108708.1	GI:13923915		
KEYWORDS		synthetic construct		
SOURCE		synthetic construct		
ORGANISM		synthetic construct		

